

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/530,910
Source: FWP
Date Processed by STIC: 8/3/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/530, 910

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 J Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 08/03/2006

PATENT APPLICATION: US/10/530,910

TIME: 09:12:22

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08032006\J530910.raw

see pp 1-5

6 <110> APPLICANT: SCHRENZEL, Jacques
 7 FRANCOIS, Patrice
 8 CHARBONNIER, Yvan
 9 JACQUET, Jean
 10 UTINGER, Dominic
 11 KRESBACH, Gerhard
 12 ABEL, Andreas
 13 EHRAT, Markus
 15 <120> TITLE OF INVENTION: Analytical chip with an array of immobilized specific
 recognition elements
 16 for the determination of clinically relevant bacteria and analytical method
 17 based thereon
 19 <130> FILE REFERENCE: 2005-0613A/WMC/01841
 21 <140> CURRENT APPLICATION NUMBER: 10/530,910
 22 <141> CURRENT FILING DATE: 2005-04-08
 24 <150> PRIOR APPLICATION NUMBER: 02022631.2-1223
 25 <151> PRIOR FILING DATE: 2002-10-09
 27 <160> NUMBER OF SEQ ID NOS: 288

see item 2
 on Euro summary
 ↓ sheet

Does Not Comply
 Corrected Diskette Needed

suggestion: Consult
 Sequence Rules
 for valid format.

ERRORED SEQUENCES

29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 19
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial Sequence
 W--> 33 <220> **FEATURE:** insert <2207 whenever <2217, <2227, or <2237 is shown
 33 <223> OTHER INFORMATION: Probe for Enterobacter cloacae
 E--> 35 <400> SEQUENCE: 1
 E--> 37 acgtcaattg ctgcgggtta
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 19
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Artificial Sequence
 W--> 44 <220> **FEATURE:** insert <2207
 44 <223> OTHER INFORMATION: Probe for Staphylococcus aureus
 E--> 46 <400> SEQUENCE: 2
 E--> 48 agcaagcttc tgcgtcgtt
 130 <210> SEQ ID NO: 19
 131 <211> LENGTH: 19
 132 <212> TYPE: DNA
 133 <213> ORGANISM: Artificial Sequence
 W--> 135 <220> **FEATURE:** insert <2207
 135 <223> OTHER INFORMATION: Probe for Escherichia coli

19 ← insert cumulative
 base total at right margin
 of each line (another
 global
 erra)

<2207 never has a
 response. It is
 a "header" only.
 (global
 erra)

19 ←

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Input Set : A:\PTO.RJ.txt

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```

E--> 137 <400> SEQUENCE: 19
E--> 139 agcaagccct tctgctggt
141 <210> SEQ ID NO: 20
142 <211> LENGTH: 19
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
W--> 146 <220> FEATURE:
146 <223> OTHER INFORMATION: Probe for Escherichia coli
E--> 148 <400> SEQUENCE: 20
E--> 150 ggcagtctct ctttgagtt
152 <210> SEQ ID NO: 21
153 <211> LENGTH: 19
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
W--> 157 <220> FEATURE:
157 <223> OTHER INFORMATION: Probe for Escherichia coli
E--> 159 <400> SEQUENCE: 21
E--> 161 tcagactacg cagcacttt
163 <210> SEQ ID NO: 22
164 <211> LENGTH: 19
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
W--> 168 <220> FEATURE:
168 <223> OTHER INFORMATION: Probe for Enterococcus faecalis
E--> 170 <400> SEQUENCE: 22
E--> 172 gccatgcggc ataaactgt
174 <210> SEQ ID NO: 23
175 <211> LENGTH: 19
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
W--> 179 <220> FEATURE:
179 <223> OTHER INFORMATION: Probe for Enterococcus faecalis
E--> 181 <400> SEQUENCE: 23
E--> 183 cgaaagcgcc tttcactct
185 <210> SEQ ID NO: 24
186 <211> LENGTH: 19
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
W--> 190 <220> FEATURE:
190 <223> OTHER INFORMATION: Probe for Enterococcus faecalis
E--> 192 <400> SEQUENCE: 24
E--> 194 agataccgtc aggggacgt
196 <210> SEQ ID NO: 25
197 <211> LENGTH: 19
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
W--> 201 <220> FEATURE:
201 <223> OTHER INFORMATION: Probe for Klebsiella pneumoniae
E--> 203 <400> SEQUENCE: 25

```

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08032006\J530910.raw

```

E--> 205 ttctctcccca ctgaaagtg
      207 <210> SEQ ID NO: 26
      208 <211> LENGTH: 19
      209 <212> TYPE: DNA
      210 <213> ORGANISM: Artificial Sequence
W--> 212 <220> FEATURE:
      212 <223> OTHER INFORMATION: Probe for Klebsiella pneumoniae
E--> 214 <400> SEQUENCE: 26
E--> 216 ggtaacgtca atcgccaag
      218 <210> SEQ ID NO: 27
      219 <211> LENGTH: 19
      220 <212> TYPE: DNA
      221 <213> ORGANISM: Artificial Sequence
W--> 223 <220> FEATURE:
      223 <223> OTHER INFORMATION: Probe for Klebsiella pneumoniae
E--> 225 <400> SEQUENCE: 27
E--> 227 tgcgggtaac gtcaatcgc
      229 <210> SEQ ID NO: 28
      230 <211> LENGTH: 19
      231 <212> TYPE: DNA
      232 <213> ORGANISM: Artificial Sequence
W--> 234 <220> FEATURE:
      234 <223> OTHER INFORMATION: Probe for Staphylococcus epidermidis (excludes
Staphylococcus aureus) → move over
E--> 236 <400> SEQUENCE: 28
E--> 238 tcactattga accatgcgg
      240 <210> SEQ ID NO: 29
      241 <211> LENGTH: 19
      242 <212> TYPE: DNA
      243 <213> ORGANISM: Artificial Sequence
W--> 245 <220> FEATURE:
      245 <223> OTHER INFORMATION: Probe for Staphylococcus aureus (excludes Staphylococcus
epidermidis) →
E--> 247 <400> SEQUENCE: 29
E--> 249 ccgtcaagat gtgcacagt
      251 <210> SEQ ID NO: 30
      252 <211> LENGTH: 19
      253 <212> TYPE: DNA
      254 <213> ORGANISM: Artificial Sequence
W--> 256 <220> FEATURE:
      256 <223> OTHER INFORMATION: Probe for Pseudomonas aeruginosa
E--> 258 <400> SEQUENCE: 30
E--> 260 gatccccac tttctccct
      262 <210> SEQ ID NO: 31
      263 <211> LENGTH: 19
      264 <212> TYPE: DNA
      265 <213> ORGANISM: Artificial Sequence
W--> 267 <220> FEATURE:
      267 <223> OTHER INFORMATION: Probe for Streptococcus pneumoniae
E--> 269 <400> SEQUENCE: 31
E--> 271 tgtcatgcaa catccactc

```

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08032006\J530910.raw

273 <210> SEQ ID NO: 32
274 <211> LENGTH: 19
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
W--> 278 <220> FEATURE:
278 <223> OTHER INFORMATION: Probe for Streptococcus pneumoniae
E--> 280 <400> SEQUENCE: 32
E--> 282 cgtgaacgta gtgatggtc 196
284 <210> SEQ ID NO: 33
285 <211> LENGTH: 19
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
W--> 289 <220> FEATURE:
289 <223> OTHER INFORMATION: Probe for Propionibacterium acnes
E--> 291 <400> SEQUENCE: 33
E--> 293 tttcaaagcc gccaaacccc 196
295 <210> SEQ ID NO: 34
296 <211> LENGTH: 19
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
W--> 300 <220> FEATURE:
300 <223> OTHER INFORMATION: Probe for Pseudomonas aeruginosa
E--> 302 <400> SEQUENCE: 34
E--> 304 gcggtattag cgcccgttt 196
306 <210> SEQ ID NO: 35
307 <211> LENGTH: 19
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
W--> 311 <220> FEATURE:
311 <223> OTHER INFORMATION: Probe for Pseudomonas aeruginosa
E--> 313 <400> SEQUENCE: 35
E--> 315 actttctccc tcaggacgt 196
317 <210> SEQ ID NO: 36
318 <211> LENGTH: 19
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
W--> 322 <220> FEATURE:
322 <223> OTHER INFORMATION: Probe for Propionibacterium acnes
E--> 324 <400> SEQUENCE: 36
E--> 326 cccacaaaag cagggcctt 196

These errors are also in subsequent sequences

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\08032006\J530910.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 15

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08032006\J530910.raw

L:33 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:35 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:37 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:1
L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:46 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:2
L:53 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (3) SEQUENCE:
L:58 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (4) SEQUENCE:
L:63 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:68 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:73 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:78 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:83 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:88 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:93 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:98 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:103 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:108 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:113 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:118 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:123 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:128 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:135 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:137 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:19
L:139 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:19
L:146 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:148 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:20
L:150 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:20
L:157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:159 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:21
L:161 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:21
L:168 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:170 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:22
L:172 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:22
L:179 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:181 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:23
L:183 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:23
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:192 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:24
L:194 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:24
L:201 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:203 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25
L:205 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:25
L:212 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:214 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26
L:216 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:26
L:223 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:225 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27

VERIFICATION SUMMARY

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Input Set : A:\PTO.RJ.txt

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L:227 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:27
L:234 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:236 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:28
L:238 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:28
L:245 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:247 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29
L:249 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:29
L:256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:258 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:30
L:260 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:30
L:267 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
L:269 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31
L:271 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:31
L:278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:280 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:32
L:282 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:32
L:289 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:291 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:33
L:293 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:33
L:300 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:302 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:34
L:304 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:34
L:311 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:313 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:35
L:315 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:35
L:322 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:324 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:36
L:326 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:36
L:333 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37
L:335 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:37
L:337 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:37
L:344 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:38
L:346 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:38
L:348 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:38
L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:39
L:357 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:39
L:359 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:39
L:366 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:40
L:368 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:40
L:370 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:40
L:377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41
L:379 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:41
L:381 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:41
L:388 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:390 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:42
L:392 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:42
L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43
L:401 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:43
L:403 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:43

VERIFICATION SUMMARY

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08032006\J530910.raw

L:410 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:44
L:412 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:44
L:414 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:44
L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:45
L:423 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:45
L:425 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:45
L:432 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:46
L:434 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46
L:436 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:46
L:443 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:47
L:445 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:47
L:447 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:47
L:454 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:48
L:456 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:48
L:458 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:48
L:465 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:49
L:467 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:49
L:469 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:49
L:476 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:50
L:478 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:50
L:480 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:50
L:487 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:51
L:489 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:51
L:491 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:51
L:498 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:52
L:500 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:52
L:502 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:52
L:509 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:53
L:511 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:53
L:513 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:53
L:520 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:54
L:522 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:54
L:524 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:54
L:531 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:55
L:533 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:55
L:535 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:55
L:542 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:56
L:544 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:56
L:546 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:56
L:553 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:57
L:555 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:57
L:557 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:57
L:564 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:58
L:566 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:58
L:568 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:58
L:575 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:59
L:577 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:59
L:579 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:59
L:586 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:60

VERIFICATION SUMMARY

DATE: 08/03/2006

PATENT APPLICATION: US/10/530,910

TIME: 09:12:23

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08032006\J530910.raw

L:588 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:60
L:590 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:60
L:597 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:61
L:599 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:61
L:601 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:61
L:608 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:62
L:610 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:62
L:612 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:62
L:619 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:63
L:621 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:63
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:63
L:630 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:64
L:632 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:64
L:634 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:64
L:641 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:65
L:643 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:65
L:645 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:65
L:652 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:66
L:654 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:66
L:656 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:66
L:2168 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (204) SEQUENCE:
L:2714 M:283 W: Missing Blank Line separator, <400> field identifier